

What is claimed is:

1. A method for identifying a potentially transcribed region of a genome comprising:

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- sub (2)
- a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample,  
wherein said nucleic acid sample comprises transcripts from said genome,  
wherein said probes are targeting an area of said genome; and
- b) Identifying said transcribed region as a region of said genome where  
hybridization of all consecutive probes targeting said region are above a  
threshold value.

10 2. The method of Claim 1 wherein said probes are oligonucleotides.

3. The method of Claim 2 wherein said oligonucleotides are immobilized on a  
substrate.

4. The method of Claim 1 wherein said threshold value is non-specific binding.

15 5. The method of Claim 4 wherein said non-specific binding is measured using a  
probe designed to contain at least one mismatched base.

6. The method of Claim 1 further comprising identifying a sub-region wherein  
hybridization of said probes targeting said sub-regions is similar and indicating  
said sub-region as said transcribed region.

7. The method of Claim 6 wherein said genome is from a prokaryote.

20 8. The method of Claim 7 wherein said transcribed region is an operon.

9. The method of Claim 8 wherein said prokaryote is E. Coli.

10. A computer software product comprising:

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